

Applicants have repeated the amendments requested in the Preliminary Amendment with reference to the paragraph numbers included in the substitute specification. Applicants respectfully request the entry of these amendments.

The Claims Are Supported by the Specification

The Examiner rejected claim 26 as allegedly containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. *Id.*, page 3. The Examiner states that, except for the glycine at position 28, all of the amino acids recited by claim 26 are identical to those found in SEQ ID NO: 1. *Id.* According to the Examiner, there is no literal support for a glycine residue at position 28. *Id.*, page 4. The Examiner concludes that claim 26 presents new matter.

Applicants respectfully traverse, but, in order to expedite prosecution, have cancelled claim 26 without prejudice or disclaimer. Applicants have added claims 43-46 to more particularly point out and distinctly claim certain embodiments of their invention. Support for the presence of amino acids other than those found in SEQ ID NO: 1 at positions 28, 43, 48, 111, 125, and 128 is found, for example, in the cDNA sequences SEQ ID NOs: 6 and 7. For example, the protein encoded by SEQ ID NO: 7 has an asparagine at position 28, a methionine at position 43, a glutamine at position 48, an arginine at position 111, a cysteine at position 125, and a phenylalanine at position 128.

The Claims Are Definite

The Examiner also rejected claim 26 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite. Office Action, page 4. According to the Examiner, the

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recitation in claim 26 that the claim proteins "comprise" SEQ ID NO: 1 contradicts the recitation in claim 25 that the proteins "consist[] essentially of" SEQ ID NO: 1. *Id.*

Without acquiescing in the rejection, Applicants have cancelled claim 26 and added new claim 43, which recites "protein consisting essentially of an amino acid sequence."

The Examiner also contends that claim 26 is indefinite in its recitation of a protein that "'further comprises' specific residues at particular positions of SEQ ID NO: 1." *Id.* According to the Examiner, "it is unclear how SEQ ID NO: 1 can 'further' comprise specific amino acid residues at particular positions of SEQ ID NO: 1 when those residues are already present in SEQ ID NO: 1." *Id.*

Without acquiescing in the rejection, Applicants have cancelled claim 26 and added independent claim 43 rendering this rejection moot.

The Claims Are Not Anticipated

The Examiner rejected claim 25 under 35 U.S.C. § 102(b) as allegedly being anticipated by Stricklin et al., J. Biol. Chem. 258: 12252-12258, 1983 ("Stricklin"). Office Action, page 5. According to the Examiner, Stricklin reports the purification of a collagenase inhibitor from human skin fibroblasts, which comprises the NH₂-terminal 25 amino acids of SEQ ID NO: 1. *Id.* The Examiner cites Carmichael et al., Proc. Natl. Acad. Sci. USA 83: 2407-2411, 1986, as evidence that the protein of SEQ ID NO: 1 is the same as the protein purified by Stricklin. *Id.*

Without acquiescing in the rejection, Applicants have amended claim 25. The proteins encompassed by the amended claim all include NH₂-terminal amino acids in addition to those reported by Stricklin and are not anticipated by that reference.

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Applicants respectfully request withdrawal of the rejection of claim 25 under 35 U.S.C. § 102(b).

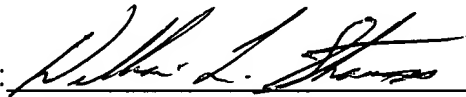
Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the application.

Please grant any extensions of time required to enter this response and charge any additional required fees to Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

Dated: July 1, 2003

By: 
William L. Strauss
Reg. No. 47,114

APPENDIX TO AMENDMENT OF JULY 1, 2003
VERSION WITH MARKINGS TO SHOW CHANGES MADE

Amendments to the Specification

Paragraph [016]:

--[016] The coding strand of a first preferred DNA sequence which has been discovered has the following nucleotide sequence (SEQ ID No: 5):

| | | | | | |
|------------|------------|------------|------------|-------------|-------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GTTGTTGCTG | TGGCTGATAG | CCCCAGCAGG | GCCTGCACCT | GTGTCCCACC | CCACCCACAG |
| 70 | 80 | 90 | 100 | 110 | 120 |
| ACGGCCTTCT | GCAATTCCGA | CCTCGTCATC | AGGGCCAAGT | TCGTGGGGAC | ACCAGAAGTC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| AACCAGACCA | CCTTATACCA | GCGTTATGAG | ATCAAGATGA | CCAAGATGTA | TAAAGGGTTC |
| 190 | 200 | 210 | 220 | 230 | 240 |
| CAAGCCTTAG | GGGATGCCGC | TGACATCCGG | TTCGTCTACA | CCCCCGCCAT | GGAGAGTGTC |
| 250 | 260 | 270 | 280 | 290 | 300 |
| TGCGGATACT | TCCACAGGTC | CCACAACCGC | AGCGAGGAGT | TTCTCATTCG | TGGAAAAGTC |
| 310 | 320 | 330 | 340 | 350 | 360 |
| CAGGATGGAC | TCTTGACAT | CACTACCTGC | AGTTTCGTGG | CTCCCTGGAA | CAGCCTGAGC |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTAGCTCAGC | GCCGGGGCTT | CACCAAGACC | TACACTGTTG | GCTGTGAGGA | ATGCACAGTG |
| 430 | 440 | 450 | 460 | 470 | 480 |
| TTTCCCTGTT | TATCCATCCC | CTGCAAACTG | CAGAGTGGCA | CTCATTGCTT | GTGGACGGAC |
| 490 | 500 | 510 | 520 | 530 | 540 |
| CAGCTCCTCC | AAGGCTCTGA | AAAGGGCTTC | CAGTCCCGTC | ACCTTGCCCTG | CCTGCCCTCGG |
| 550 | 560 | 570 | 580 | 590 | 600 |
| GAGCCAGGGC | TGTGCACCTG | GCAGTCCCTG | CGGTCCCAGA | TAGCCTGAAT | CCTGCCCCGA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| GTGGAAGCTG | AAGCCTGCAC | AGTGTCCACC | CTGTTCCCAC | TCCCATCTTT | CTTCCGGACA |

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670 680 690 700
 ATGAAATAAA GAGTTACCAC CCAGCAAAAA AAAAAAGGAA TTC--

Paragraph [018]:

--[018] A second preferred DNA sequence has been discovered which has an additional nucleotide sequence 5' to the initiator sequence. This sequence, which contains as the eighty-second through four-hundred-thirty-second nucleotides nucleotides 1 through 351 of the first preferred sequence set forth above, has the following nucleotide sequence (SEQ ID No: 6):

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GGCCATCGCC | GCAGATCCAG | CGCCCAGAGA | GACACCAGAG | AACCCACCAT | GGCCCCCTTT |
| 70 | 80 | 90 | 100 | 110 | 120 |
| GACCCCTGGC | TTCTGCATCC | TGTTGTTGCT | GTGGCTGATA | GCCCCAGCAG | GGCCTGCACC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| TGTGTCCCAC | CCCACCCACA | GACGGCCTTC | TGCAATTCCG | ACCTCGTCAT | CAGGGCCAAG |
| 190 | 200 | 210 | 220 | 230 | 240 |
| TTCGTGGGGA | CACCAGAAGT | CAACCAGACC | ACCTTATACC | AGCGTTATGA | GATCAAGATG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| ACCAAGATGT | ATAAAGGGTT | CCAAGCCTTA | GGGGATGCCG | CTGACATCCG | GTTCGTCTAC |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ACCCCCGCCA | TGGAGAGTGT | CTGCGGATAC | TTCCACAGGT | CCCACAACCG | CAGCGAGGAG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTTCTCATTG | CTGGAAACT | GCAGGATGGA | CTCTTGACAC | TCACTACCTG | CAGTTTCGTG |
| 430 | | | | | |
| GCTCCCTGGA | AC-- | | | | |

Paragraph [019]:

--[019] A third preferred DNA sequence which incorporates the 5' region of the second preferred sequence and the 3' sequence of the first preferred sequence, has the following nucleotide sequence (SEQ ID No: 7):

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| | | | | | |
|------------|-------------|------------|-------------|-------------|--------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GGCCATCGCC | GCAGATCCAG | CGCCCAGAGA | GACACCAGAG | AACCCACCAT | GGCCCCCTTT |
| 70 | 80 | 90 | 100 | 110 | 120 |
| GACCCCTGGC | TTCTGCATCC | TGTTGTTGCT | GTGGCTGATA | GCCCCAGCAG | GGCCTGCACC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| TGTGTCCCAC | CCCACCCACA | GACGGCCTTC | TGCAATTCCG | ACCTCGTCAT | CAGGGCCAAG |
| 190 | 200 | 210 | 220 | 230 | 240 |
| TTCGTGGGGA | CACCAGAAGT | CAACCAGACC | ACCTTATACC | AGCGTTATGA | GATCAAGATG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| ACCAAGATGT | ATAAAGGGTT | CCAAGCCTTA | GGGGATGCCG | CTGACATCCG | GTTTCGTCTAC |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ACCCCCGCCA | TGGAGAGTGT | CTGCGGATAC | TTCCACAGGT | CCCACAACCG | CAGCGAGGAG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTTCTCATTG | CTGGA AAACT | GCAGGATGGA | CTCTTG CACA | TCACTACCTG | CAGTTTCGTG |
| 430 | 440 | 450 | 460 | 470 | 480 |
| GCTCCCTGGA | ACAGCCTGAG | CTTAGCTCAG | CGCCGGGGCT | TCACCAAGAC | CTACACTGTT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| GGCTGTGAGG | AATGCACAGT | GTTTCCCTGT | TTATCCATCC | CCTGCAA ACT | GCAGAGTGGC |
| 550 | 560 | 570 | 580 | 590 | 600 |
| ACTCATTGCT | TGTGGACGGA | CCAGCTCCTC | CAAGGCTCTG | AAAAGGGGCT | CCAGTCCCGT |
| 610 | 620 | 630 | 640 | 650 | 660 |
| CACCTTGCCT | GCCTGCCTCG | GGAGCCAGGG | CTGTGCACCT | GGCAGTCCCT | GCGGTCCCAG |
| 670 | 680 | 690 | 700 | 710 | 720 |
| ATAGCCTGAA | TCCTGCCCCG | AGTGGAAGCT | GAAGCCTGCA | CAGTGTCCAC | CCTGTTCCCA |
| 730 | 740 | 750 | 760 | 770 | 780 |
| CTCCCATCTT | TCTTCCGGAC | AATGAAATAA | AGAGTTACCA | CCCAGCAAAA | AAAAAAAGGA-- |

Paragraph [030]:

--[030] A first preferred portable DNA sequence of the present invention has a nucleotide sequence SEQ ID No: 5 as follows:

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GTTGTTGCTG | TGGCTGATAG | CCCCAGCAGG | GCCTGCACCT | GTGTCCCACC | CCACCCACAG |
| 70 | 80 | 90 | 100 | 110 | 120 |
| ACGGCCTTCT | GCAATTCCGA | CCTCGTCATC | AGGGCCAAGT | TCGTGGGGAC | ACCAGAAGTC |

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| | | | | | |
|------------|------------|-------------|------------|-------------|------------|
| 130 | 140 | 150 | 160 | 170 | 180 |
| AACCAGACCA | CCTTATACCA | GCGTTATGAG | ATCAAGATGA | CCAAGATGTA | TAAAGGGTTC |
| 190 | 200 | 210 | 220 | 230 | 240 |
| CAAGCCTTAG | GGGATGCCGC | TGACATCCGG | TTCGTCTACA | CCCCCGCCAT | GGAGAGTGTC |
| 250 | 260 | 270 | 280 | 290 | 300 |
| TGCGGATACT | TCCACAGGTC | CCACAACCGC | AGCGAGGAGT | TTCTCATTGC | TGGAAAACTG |
| 310 | 320 | 330 | 340 | 350 | 360 |
| CAGGATGGAC | TCTTGACAT | CACTACCTGC | AGTTTCGTGG | CTCCCTGGAA | CAGCCTGAGC |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTAGCTCAGC | GCCGGGGCTT | CACCAAGACC | TACACTGTTG | GCTGTGAGGA | ATGCACAGTG |
| 430 | 440 | 450 | 460 | 470 | 480 |
| TTTCCCTGTT | TATCCATCCC | CTGCAAACCTG | CAGAGTGGCA | CTCATTGCTT | GTGGACGGAC |
| 490 | 500 | 510 | 520 | 530 | 540 |
| CAGCTCCTCC | AAGGCTCTGA | AAAGGGCTTC | CAGTCCCGTC | ACCTTGCCCTG | CCTGCCTCGG |
| 550 | 560 | 570 | 580 | 590 | 600 |
| GAGCCAGGGC | TGTGCACCTG | GCAGTCCCTG | CGGTCCCAGA | TAGCCTGAAT | CCTGCCCGGA |
| 610 | 620 | 630 | 640 | 650 | 660 |
| GTGGAAGCTG | AAGCCTGCAC | AGTGTCCACC | CTGTTCCCAC | TCCCATCTTT | CTTCCGGACA |
| 670 | 680 | 690 | 700 | | |
| ATGAAATAAA | GAGTTACCAC | CCAGCAAAAA | AAAAAAGGAA | TTC-- | |

Paragraph [031]:

--[031] A second preferred portable DNA sequence of the present invention has the following nucleotide sequence (SEQ ID No: 6):

| | | | | | |
|------------|------------|------------|------------|------------|-------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GGCCATCGCC | GCAGATCCAG | CGCCCAGAGA | GACACCAGAG | AACCCACCAT | GGCCCCCTTT |
| 70 | 80 | 90 | 100 | 110 | 120 |
| GACCCCTGGC | TTCTGCATCC | TGTTGTTGCT | GTGGCTGATA | GCCCCAGCAG | GGCCTGCACC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| TGTGTCCCAC | CCCACCCACA | GACGGCCTTC | TGCAATTCCG | ACCTCGTCAT | CAGGGCCAAG |
| 190 | 200 | 210 | 220 | 230 | 240 |
| TTCGTGGGGA | CACCAGAAGT | CAACCAGACC | ACCTTATACC | AGCGTTATGA | GATCAAGATG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| ACCAAGATGT | ATAAAGGGTT | CCAAGCCTTA | GGGGATGCCG | CTGACATCCG | GTTTCGTCTAC |

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| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 310 | 320 | 330 | 340 | 350 | 360 |
| ACCCCCGCCA | TGGAGAGTGT | CTGCGGATAC | TTCCACAGGT | CCCACAACCG | CAGCGAGGAG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTTCTCATTG | CTGGAAAACT | GCAGGATGGA | CTCTTGCACA | TACTACCTG | CAGTTTCGTG |
| 430 | | | | | |
| GCTCCCTGGA | AC-- | | | | |

Paragraph [033]:

--[033] A third preferred portable DNA sequence has the nucleotide sequence

(SEQ ID No: 7):

| | | | | | |
|------------|------------|------------|------------|-------------|-------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GGCCATCGCC | GCAGATCCAG | CGCCCAGAGA | GACACCAGAG | AACCCACCAT | GGCCCCCTTT |
| 70 | 80 | 90 | 100 | 110 | 120 |
| GACCCCTGGC | TTCTGCATCC | TGTTGTTGCT | GTGGCTGATA | GCCCCAGCAG | GGCCTGCACC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| TGTGTCCCAC | CCCACCCACA | GACGGCCTTC | TGCAATTCCG | ACCTCGTCAT | CAGGGCCAAG |
| 190 | 200 | 210 | 220 | 230 | 240 |
| TTCGTGGGGA | CACCAGAAGT | CAACCAGACC | ACCTTATACC | AGCGTTATGA | GATCAAGATG |
| 250 | 260 | 270 | 280 | 290 | 300 |
| ACCAAGATGT | ATAAAGGGTT | CCAAGCCTTA | GGGGATGCCG | CTGACATCCG | GTTTCGTCTAC |
| 310 | 320 | 330 | 340 | 350 | 360 |
| ACCCCCGCCA | TGGAGAGTGT | CTGCGGATAC | TTCCACAGGT | CCCACAACCG | CAGCGAGGAG |
| 370 | 380 | 390 | 400 | 410 | 420 |
| TTTCTCATTG | CTGGAAAACT | GCAGGATGGA | CTCTTGCACA | TACTACCTG | CAGTTTCGTG |
| 430 | 440 | 450 | 460 | 470 | 480 |
| GCTCCCTGGA | ACAGCCTGAG | CTTAGCTCAG | CGCCGGGGCT | TCACCAAGAC | CTACACTGTT |
| 490 | 500 | 510 | 520 | 530 | 540 |
| GGCTGTGAGG | AATGCACAGT | GTTTCCCTGT | TTATCCATCC | CCTGCAAACCT | GCAGAGTGGC |
| 550 | 560 | 570 | 580 | 590 | 600 |
| ACTCATTGCT | TGTGGACGGA | CCAGCTCCTC | CAAGGCTCTG | AAAAGGGCTT | CCAGTCCCGT |
| 610 | 620 | 630 | 640 | 650 | 660 |
| CACCTTGCCT | GCCTGCCTCG | GGAGCCAGGG | CTGTGCACCT | GGCAGTCCCT | GCGGTCCCAG |
| 670 | 680 | 690 | 700 | 710 | 720 |
| ATAGCCTGAA | TCCTGCCCCG | AGTGGAAGCT | GAAGCCTGCA | CAGTGTCCAC | CCTGTTCCCA |

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730 740 750 760 770 780
CTCCCATCTT TCTTCCGGAC AATGAAATAA AGAGTTACCA CCCAGCAAAA AAAAAAAGGA--

Paragraph [059]:

--[059] It is anticipated that translation of mRNA coding for the metalloproteinase inhibitor in yeast will be more efficient with the preferred codon usage of yeast than with the sequence present in pUC8-Fic, as identified in Example 2, which has been tailored to the prokaryotic bias. For this reason, the portion of the 5' end of the portable DNA sequence beginning at the *Tth111I* site is preferably resynthesized. The new sequence favors the codons most frequently used in yeast. This new sequence preferably has the following nucleotide sequence:

HgiAI

(SEQ ID No: 8) 5' GAT CCG TGC ACT TGT GTT CCA CCA CAC
(SEQ ID No: 9) GC ACG TGA ACA CAA GGT GGT GTG

CCA CAA ACT GCT TTC TGT AAC TCT GAC C
GGT GTT TGA CGA AAG ACA TTG AGA CTG GA 3'--

Paragraph [075]:

--[075] In this method, the portable DNA sequences are those synthetic or naturally-occurring polynucleotides described above. In a preferred embodiment of the present method, the portable DNA sequence has the nucleotide sequence SEQ ID No: 5 as follows:

| | | | | | |
|------------|------------|------------|------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 | 60 |
| GTTGTTGCTG | TGGCTGATAG | CCCCAGCAGG | GCCTGCACCT | GTGTCCCACC | CCACCCACAG |
| 70 | 80 | 90 | 100 | 110 | 120 |
| ACGGCCTTCT | GCAATTCCGA | CCTCGTCATC | AGGGCCAAGT | TCGTGGGGAC | ACCAGAAGTC |
| 130 | 140 | 150 | 160 | 170 | 180 |
| AACCAGACCA | CCTTATACCA | GCGTTATGAG | ATCAAGATGA | CCAAGATGTA | TAAAGGGTTC |
| 190 | 200 | 210 | 220 | 230 | 240 |
| CAAGCCTTAG | GGGATGCCGC | TGACATCCGG | TTCGTCTACA | CCCCCGCCAT | GGAGAGTGTC |

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      250      260      270      280      290      300
TGCGGATACT TCCACAGGTC CCACAACCGC AGCGAGGAGT TTCTCATTGC TGGAAAAC TG

      310      320      330      340      350      360
CAGGATGGAC TCTTGACAT CACTACCTGC AGTTTCGTGG CTCCCTGGAA CAGCCTGAGC

      370      380      390      400      410      420
TTAGCTCAGC GCCGGGGGCTT CACCAAGACC TACACTGTTG GCTGTGAGGA ATGCACAGTG

      430      440      450      460      470      480
TTTCCCTGTT TATCCATCCC CTGCAAACTG CAGAGTGGCA CTCATTGCTT GTGGACGGAC

      490      500      510      520      530      540
CAGCTCCTCC AAGGCTCTGA AAAGGGCTTC CAGTCCCGTC ACCTTGCCTG CCTGCCTCGG

      550      560      570      580      590      600
GAGCCAGGGC TGTGCACCTG GCAGTCCCTG CGGTCCCAGA TAGCCTGAAT CCTGCCCGGA

      610      620      630      640      650      660
GTGGAAGCTG AAGCCTGCAC AGTGTCCACC CTGTTCCCAC TCCCATCTTT CTTCCGGACA

      670      680      690      700
ATGAAATAAA GAGTTACCAC CCAGCAAAAA AAAAAAGGAA TTC--

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Paragraph [084]:

--[084] In certain circumstances, the metalloproteinase inhibitor will assume its proper, active structure upon expression in the host microorganism and transport of the protein through the cell wall or membrane into the periplasmic space. This will generally occur if DNA coding for an appropriate leader sequence has been linked to the DNA coding for the recombinant protein. The preferred [metalloprotenase] metalloproteinase inhibitors of the present invention will assume their mature, active form upon translocation out of the inner cell membrane. The structures of numerous signal peptides have been published, for example by Marion E.E. Watson in Nuc. Acid Res. [12: 515-5164] 12: 5145-5164, 1984, specifically incorporated herein by reference. It is intended that these leader sequences, together with portable DNA, will direct intracellular production of a fusion protein which will be transported through the cell

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membrane and will have the leader sequence portion cleaved upon release from the cell.--

Paragraph [0104]:

--[0104] The structure of FIBAC A is

(SEQ ID No: 10) GA TCC GCG ATC GGA GTG TAA GAA ATG TGC ACT
(SEQ ID No: 11) G CGC TAG CCT CAC ATT CTT TAC ACG TGA

TGC GTT CCG CCG CAT CCG CAG ACT GCT TTC
ACG CAA GGC GGC GTA GGC GTC TGA CGA AAG

TGC AAC TCT GAC C
ACG TTG AGA CTG GA--

Paragraph [0106]:

--[0106] Component oligonucleotide FA1 (SEQ ID No: 12) is:
GATCC GCGAT CGGAG TGTA GAAAT GTGCA CTTGC--

Paragraph [0107]:

--[0107] Component oligonucleotide FA2 (SEQ ID No: 13) is:
GGAACG CAAGT GCACA TTTCT TACAC TCCGA TCGCG--

Paragraph [0108]:

--[0108] Component oligonucleotide FA3 (SEQ ID No: 14) is:
GTTC CGCCG CATCC GCAGA CTGCT TTCTG CAACT CTGAC C--

Paragraph [0109]:

--[0109] Component oligonucleotide FA4 (SEQ ID No: 15) is:
AGGTC AGAGT TGCAG AAAGC AGTCT GCGGA TGCGG C--

Paragraph [0112]:

--[0112] Linker A1 (SEQ ID No: 16) is: AATTGGCAG--

Paragraph [0113]:

--[0113] Linker A2 (SEQ ID No: 17) is: TCGACTGCC--

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Paragraph [0116]:

--[0116] The sequence of the sense strand (SEQ ID No: 18) is:

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      10      20      30      40      50      60
GAATTCGATA TCTCGTTGGA GATATTCATG ACGTATTTTG GATGATAACG AGGCGCAAAA
E   T E                               F           M   H
C   A C                               O           N   H
O   Q O                               K           L   A
1   1 5                               1           1   1

      70      80      90      100     110
AATGAAAAAG ACAGCTATCG CGATCGCAGT GGCCTGGCT GGTTCGCTA CCGTA
      A   NF PS
      L   RN VA
      U   UU UU
      1   12 1A

    120      130
GCGCA GGCCTCTGGT AAAAGCTT
H   S H M           HA
H   T A N           IL
A   U E L           NU
1   1 3 1           31--
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Paragraph [0120]:

--[0120] Linker B1 (SEQ ID No: 19) is: GATCCCAGGCCTGCA--

Paragraph [0121]:

--[0121] Linker B2 (SEQ ID No: 20) is: GGCCTGG--

Paragraph [0136]:

--[0136] The second preferred sequence (SEQ ID No: 6) as set forth herein, i.e.,

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      10      20      30      40      50      60
GGCCATCGCC GCAGATCCAG CGCCCAGAGA GACACCAGAG AACCCACCAT GGCCCCCTTT

      70      80      90      100     110     120
GACCCCTGGC TTCTGCATCC TGTTGTTGCT GTGGCTGATA GCCCCAGCAG GGCCTGCACC

      130     140     150     160     170     180
TGTGTCCCAC CCCACCCACA GACGGCCTTC TGCAATTCCG ACCTCGTCAT CAGGGCCAAG

      190     200     210     220     230     240
TTCGTGGGGA CACCAGAAGT CAACCAGACC ACCTTATACC AGCGTTATGA GATCAAGATG

      250     260     270     280     290     300
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ACCAAGATGT ATAAAGGGTT CCAAGCCTTA GGGGATGCCG CTGACATCCG GTTCGTCTAC

310 320 330 340 350 360

ACCCCCGCCA TGGAGAGTGT CTGCGGATAC TTCCACAGGT CCCACAACCG CAGCGAGGAG

370 380 390 400 410 420

TTTCTCATTG CTGGAAACT GCAGGATGGA CTCTTGACA TCACTACCTG CAGTTTCGTG

430

GCTCCCTGGA AC--

Amendments to the Claims:

Claim 25:

25. (Amended) A purified collagenase inhibitor protein, said protein consisting essentially of an amino acid sequence selected from among the following:

[a] amino acid sequence SEQ ID NO: 1; or]

[b)a) amino acid sequence SEQ ID NO: 2; or

[c)b) the amino acid sequence[s] of a) or of SEQ ID NO: 1 [b)], further having a Met at position -1; or

[d)c) the amino acid sequence of a) or of SEQ ID NO: 1 [b)], further having a leader sequence at the N-terminal, -1 position, wherein said leader sequence consists essentially of the following amino acid sequence from positions -38 to -1:

Gly His Arg Arg Arg Ser Ser Ala Gln Arg Asp Thr Arg Glu Pro Thr
Met Ala Pro Phe Asp Pro Trp Leu Leu His Pro Val Val Ala Val Ala
Asp Ser Pro Ser Arg Ala (SEQ ID NO: 3); or

[e)d) the amino acid sequence of a) or of SEQ ID NO: 1, [b)] further having a leader sequence at the N-terminal, -1 position, wherein said leader sequence consists essentially of the following amino acid sequence from positions -22 to -1: Met Ala Pro Phe Asp Pro Trp Leu Leu His Pro Val Val Ala Val Ala Asp Ser Pro Ser Arg Ala (SEQ ID NO: 4).

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